

IT IS CLAIMED:

1. A transgenic plant comprising a plant transformation vector comprising a nucleotide sequence that encodes or is complementary to a sequence that encodes a HIO32.2 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or an ortholog thereof, whereby the transgenic plant has a high oil phenotype relative to control plants.
2. The transgenic plant of Claim 1, which is selected from the group consisting of rapeseed, soy, corn, sunflower, cotton, cocoa, safflower, oil palm, coconut palm, flax, castor and peanut.
3. A plant part obtained from the plant according to Claim 1.
4. The plant part of Claim 3, which is a seed.
5. A method of producing oil comprising growing the transgenic plant of Claim 1 and recovering oil from said plant.
6. A method of producing a high oil phenotype in a plant, said method comprising:
 - a) introducing into progenitor cells of the plant a plant transformation vector comprising a nucleotide sequence that encodes or is complementary to a sequence that encodes a HIO32.2 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or an ortholog thereof, and
 - b) growing the transformed progenitor cells to produce a transgenic plant, wherein said polynucleotide sequence is expressed, and said transgenic plant exhibits an altered oil content phenotype relative to control plants.
7. A plant obtained by a method of claim 6.
8. The plant of Claim 7, which is selected from the group consisting of rapeseed, soy, corn, sunflower, cotton, cocoa, safflower, oil palm, coconut palm, flax, castor and peanut.
9. The plant of claim 7, wherein the plant is selected from the group consisting of a plant grown from said progenitor cells, a plant that is the direct progeny of a plant grown

from said progenitor cells, and a plant that is the indirect progeny of a plant grown from said progenitor cells.

10. A method of generating a plant having a high oil phenotype comprising identifying a plant that has an allele in its *HIO32.2* gene that results in increased oil content compared to plants lacking the allele and generating progeny of said identified plant, wherein the generated progeny inherit the allele and have the high oil phenotype.

11. The method of claim 10 that employs candidate gene/QTL methodology.

12. The method of claim 10 that employs TILLING methodology.